

GenCode version 5.1.6  
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OM protein - protein search, using sw model  
Run on: July 2, 2003, 09:32:00 : Search time 99 Seconds  
166366 Million cells updated/sec

Title: np\_000123  
Perfect score: 12418  
Sequence: 1 mlaefcagfcflafcfda.....whfslarwfgceadly 2351  
Scoring table: BLOSUM62  
Gap 10.0, Expect 0.5

Total number of hits exceeding chosen parameters: 908470  
Minimum db seq length: 0  
Maximum db seq length: 200000000  
Post-processing: Minimum Match 10  
Minimum Match 10  
Listing first 5 summaries

Database: A: Genesep\_10.0021\*

No.	Score	Match	Length	DB	ID	Description
1	12418	100.0	2351	18	AA011425	Active Factor VIII
2	12418	100.0	2351	18	AA011419	Active Factor VIII
3	12418	100.0	2351	18	AA011387	Active Factor VIII
4	12418	100.0	2351	18	AA011362	Active Factor VIII
5	12418	100.0	2351	18	AA011357	Active Factor VIII
6	12418	100.0	2351	18	AA011347	Active Factor VIII
7	12418	100.0	2351	18	AA011342	Active Factor VIII
8	12418	100.0	2351	18	AA011337	Active Factor VIII
9	12418	100.0	2351	18	AA011332	Active Factor VIII
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1861 DEAFVNSGLTLPGLTSGNPTLMAKNSQVYVGFVAFPTDEETSWFTENKNGNA 1920  
 1862 ..... 1920  
 1863 DLEADNSGLTGLWCTWCTLMAKNSQVYVGFVAFPTDEETSWFTENKNGNA 1920  
 1864 ..... 1920  
 1921 PCNCHQDEPPEKMYRPAALNPTNPTDGLVMDQVDFEITLMSGNENRISLIPGRI 1980  
 1922 ..... 1980  
 1923 PCNCHQDEPPEKMYRPAALNPTNPTDGLVMDQVDFEITLMSGNENRISLIPGRI 1980  
 1924 ..... 1980  
 1981 VFFVRRKEKRYALVLTGVVEYSVMSPSADNLVWGLLGGHLMANSTLPLVSNK 2040  
 1982 ..... 2040  
 1983 VFFVRRKEKRYALVLTGVVEYSVMSPSADNLVWGLLGGHLMANSTLPLVSNK 2040  
 1984 ..... 2040  
 2041 GFTVMSNSQVDFQITNSGTCVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 2100  
 2042 ..... 2100  
 2043 GFTVMSNSQVDFQITNSGTCVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 2100  
 2044 ..... 2100  
 2101 HGFTQVMSNSQVDFQITNSGTCVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 2160  
 2102 ..... 2160  
 2103 HGFTQVMSNSQVDFQITNSGTCVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 2160  
 2104 ..... 2160  
 2161 PPIATATKLPATPSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 2220  
 2162 ..... 2220  
 2163 PPIATATKLPATPSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 2220  
 2164 ..... 2220  
 2221 TNSGSAKALVQSGNSNPNVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 2280  
 2222 ..... 2280  
 2223 TNSGSAKALVQSGNSNPNVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 2280  
 2224 ..... 2280  
 2281 TNSGSAKALVQSGNSNPNVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 2340  
 2282 ..... 2340  
 2283 TNSGSAKALVQSGNSNPNVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 2340  
 2284 ..... 2340  
 2341 RVLCGNDQIT 2351  
 2342 ..... 2351  
 2343 RVLCGNDQIT 2351  
 2344 ..... 2351

11-JUL-1995, 9925-0001025.  
 (CIR) CATION CORP.  
 Cohen FE, Hung DF, Imbs M;  
 WPI: 1997-119900/1.  
 K-7508, A073137.  
 Factor VIII:C analog modified adjacent to a non-activating Arg  
 residue used in the treatment of hemophiliacs. By improvement of  
 hemostasis  
 Diagnostics; Fig 1: 50pp; English.  
 This sequence represents the active factor VIII:C. Factor VIII:C is a  
 large glycoprotein with a catalytic site in the blood coagulation cascade  
 effecting hemostasis. A deficiency in factor VIII:C is responsible for  
 the disease hemophilia. Factor VIII:C is activated by plasma, increased bleeding  
 thrombin, during activation the mature polypeptide is cleaved to  
 produce the active factor VIII:C analogues. The active factor VIII:C  
 modified at a site adjacent to a non-activating Arg residue to form a  
 Arg-Pro or Arg-Arg dipeptide is created. Complexes of two or more of the  
 modified factor VIII:C analogues are used for the prevention or treatment of active  
 Factor VIII:C deficiency in a mammal. The analogues may be used as  
 replacement of hemostasis. The analogues are resistant to proteolytic  
 cleavage and display increased plasma half-life. They may be administered  
 at lower dosages and by different modes of administration.  
 Sequence 2351 Aa.  
 Query Match 100.0%; Score 12418; Dn 18; Length 2351.  
 Blast Local Statistics 100.0%; Pval No. 0;  
 Matches 2351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MOETSTFCFLALNCTSNRYTGLAVLMDNGSDGLPDLAPFPSPSP 60  
 2 MOETSTFCFLALNCTSNRYTGLAVLMDNGSDGLPDLAPFPSPSP 60  
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 51 TSNVYATLWTFVDFPNTAPSPNMGILDTPTLQAVTDTVTLMASPRELAV 120  
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17-MOV-1997 (first entry)  
 Active Factor VIII:C analogue 5234.  
 Factor VIII:C analogues; glycoproteins; blood coagulation cascade;  
 fibrinogen; fibrin clots; haemostasis; haemophilia A; bleeding diathesis;  
 plasma procedures; thrombosis; immunogen; antibody; haemophilic; therapy;  
 protein; cell cleavage.  
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 Key: Location/Qualifiers  
 Peptide /note="Signal peptide"  
 Protein 20..215  
 Region 20..215  
 /note="Structure Factor VIII:C"  
 /note="heavy chain fragment"  
 Modified site /label="Phe, Glu, Pro  
 Region 1668..2350  
 /note="1667-1918c chain fragment"  
 Domain 760..1667  
 /note="\* domain"  
 MOV970195-A1.  
 30-JAN-1997.  
 09-JUL-1996; 96MO-US11444.  
 11-JUL-1995; 95DS-0001025.  
 (CHIR ) CHIRON CORP.  
 Cohen FE, Hung DF, Inals M;  
 WPI; 1997-110900/11.  
 Factor VIII:C analog modified adjacent to a non-activating Arg  
 residue used in the treatment of haemophilia; by improvement of  
 haemostasis  
 Claim 10; Page 1; 90pp; English.  
 AM1130-4147 represent active Factor VIII:C analogues of the  
 human factor VIII:C. The analogues are prepared by the Factor  
 VIII:C coding sequence (see AM1357) using mutagenic primers. The  
 analogues comprise a native Factor VIII:C polypeptide modified at a site  
 adjacent to the active site. The analogues are prepared by the active  
 dipeptide is created. Factor VIII:C is a large glycoprotein that  
 participates in the blood coagulation cascade that ultimately converts  
 fibrinogen to fibrin. Factor VIII:C is responsible for hemophilia A, which is an  
 X-chromosome-linked inherited bleeding diathesis. Factor VIII:C is the  
 active polypeptide is cleaved to generate heavy and light chain fragments  
 that are further cleaved. Complexes of two or more of the analogues,  
 which are prepared by the Factor VIII:C coding sequence, are used for  
 Factor VIII:C deficiency in a mammal. The analogues may be used as a  
 coagulation with each other for the prevention or treatment of active  
 haemophilia. The analogues are resistant to proteolytic  
 cleavage and display increased plasma half-life. They may be administered  
 at lower dosages and by different modes of administration.  
 Sequence 2351 AA;  
 Query Match 100.0%; Score 12414; DB 18; Length 2351;  
 Beat Local Similarly 100.0%; Pred. No. 1; Indels 0; Gaps 0;  
 Matches 2350; Conservative 0; Mismatches

1 MOV130-4147 represent active Factor VIII:C analogues of the  
 human factor VIII:C. The analogues are prepared by the Factor  
 VIII:C coding sequence (see AM1357) using mutagenic primers. The  
 analogues comprise a native Factor VIII:C polypeptide modified at a site  
 adjacent to the active site. The analogues are prepared by the active  
 dipeptide is created. Factor VIII:C is a large glycoprotein that  
 participates in the blood coagulation cascade that ultimately converts  
 fibrinogen to fibrin. Factor VIII:C is responsible for hemophilia A, which is an  
 X-chromosome-linked inherited bleeding diathesis. Factor VIII:C is the  
 active polypeptide is cleaved to generate heavy and light chain fragments  
 that are further cleaved. Complexes of two or more of the analogues,  
 which are prepared by the Factor VIII:C coding sequence, are used for  
 Factor VIII:C deficiency in a mammal. The analogues may be used as a  
 coagulation with each other for the prevention or treatment of active  
 haemophilia. The analogues are resistant to proteolytic  
 cleavage and display increased plasma half-life. They may be administered  
 at lower dosages and by different modes of administration.  
 Sequence 2351 AA;  
 Query Match 100.0%; Score 12414; DB 18; Length 2351;  
 Beat Local Similarly 100.0%; Pred. No. 1; Indels 0; Gaps 0;  
 Matches 2350; Conservative 0; Mismatches

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[illegible][illegible]



Wed Jul 2 11:12:40 2003

np\_000123.rag

Page 25

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Db 1861  GQSPHOLVSLKDEYQANLSSKNKYNVYVLTNORHMYNMLALN 1860
Oy 1921  GQSPHOLVSLKDEYQANLSSKNKYNVYVLTNORHMYNMLALN 1920
Db 1921  GQSPHOLVSLKDEYQANLSSKNKYNVYVLTNORHMYNMLALN 1920

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Oy 1921  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 1980
Db 1921  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 1980
Oy 1981  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 1980
Db 1981  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 1980
Oy 2041  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 2040
Db 2041  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 2040
Oy 2101  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 2100
Db 2101  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 2100
Oy 2161  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 2160
Db 2161  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 2160
Oy 2221  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 2220
Db 2221  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 2220
Oy 2281  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 2280
Db 2281  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 2280
Oy 2341  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 2340
Db 2341  PCDNQDQDPTFENREHNTNQLNQLDQDQDQDQDQDQDQDQDQDQDQD 2340

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RESULT 4
542220-1
? Patient No: 542220
? TITLE OF ANNOTATION: HUMAN FACTOR VARI C MAPPING
? NUMBER OF SEQUENCES: 15
? CURRENT APPLICATION DATA: 07/083,936
? FILLING DATE: 15-MAY-1992
? FILLING DATE: 02-DEC-1986; 09-DEC-1986
? APPLICATION NUMBER: 935,698
? FILLING DATE: 18-NOV-1986
? FILLING DATE: 29-MAY-1986
? SBD TO NO.1:
542220-1

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Query Match 38.8% Score 1236; df 6; length 2351;
Matches 3348; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 181. VEDVJEDJMSGLJALLVNCBRSJLANKVOTJLRFJLLAVTDOJESHSJSTJMSJLMDJ 240
Oy 241. AASABRPMPTVYVWVMSJ-POLJGJCRKSHVWVHJGCTTSPVNSJFJESJFVJFVNN 300
Db 241. AASABRPMPTVYVWVMSJ-POLJGJCRKSHVWVHJGCTTSPVNSJFJESJFVJFVNN 300
Oy 301. ROLESJISJFJFJOTJLMDJGJFJLJFJHSJDSJHJWVHJGCTTSPVNSJFJESJFVJFVNN 350
Db 301. ROLESJISJFJFJOTJLMDJGJFJLJFJHSJDSJHJWVHJGCTTSPVNSJFJESJFVJFVNN 350
Oy 351. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 420
Db 351. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 420
Oy 421. PDDJSTJESJOTJNMDJOTJGJFJHJWVHJGCTTSPVNSJFJESJFVJFVNN 480
Db 421. PDDJSTJESJOTJNMDJOTJGJFJHJWVHJGCTTSPVNSJFJESJFVJFVNN 480
Oy 481. LITJFJHJNSJFJOTJNMDJOTJGJFJHJWVHJGCTTSPVNSJFJESJFVJFVNN 540
Db 481. LITJFJHJNSJFJOTJNMDJOTJGJFJHJWVHJGCTTSPVNSJFJESJFVJFVNN 540
Oy 541. TKSJDPJCRJFJISJFJHJWVHJGCTTSPVNSJFJESJFVJFVNN 600
Db 541. TKSJDPJCRJFJISJFJHJWVHJGCTTSPVNSJFJESJFVJFVNN 600
Oy 601. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 660
Db 601. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 660
Oy 661. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 720
Db 661. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 720
Oy 721. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 780
Db 721. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 780
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Db 781. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 840
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Oy 1021. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1080
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Oy 1081. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1140
Db 1081. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1140
Oy 1141. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1200
Db 1141. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1200
Oy 1201. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1260
Db 1201. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1260
Oy 1261. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1320
Db 1261. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1320

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Db 1261. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1320
Oy 1321. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1380
Db 1321. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1380
Oy 1381. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1440
Db 1381. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1440
Oy 1441. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1500
Db 1441. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1500
Oy 1501. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1560
Db 1501. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1560
Oy 1561. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1620
Db 1561. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1620
Oy 1621. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1680
Db 1621. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1680
Oy 1681. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1740
Db 1681. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1740
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Db 1741. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1800
Oy 1801. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1860
Db 1801. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1860
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Db 1861. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1920
Oy 1921. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1980
Db 1921. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 1980
Oy 1981. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 2040
Db 1981. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 2040
Oy 2041. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 2100
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Oy 2281. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 2340
Db 2281. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 2340
Oy 2341. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 2400
Db 2341. JENJVDJOTJESJDMVJFJODJMSJFJOTJSHJAKJHJWVHJGCTTSPVNSJFJESJFVJFVNN 2400

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RESULT 5
Sequence 4 Application US/078640048
Patent No. 5564771
GENERAL INFORMATION:
APPLICANT: Sange, Marshall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
ADDRESS: K11Patrick & Cody
CORRESPONDENCE ADDRESS:
CITY: Atlanta
STATE: Georgia
COUNTRY: US
COMPLET RESOLUBLE FORM:
MEDIAN TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Piletrin Release #1.0, Version #1.25
COMPLET APPLICATION DATA: 07/06/0048
FILING DATE: 07 APRIL 1992
CLASSIFICATION: 433
NAME: Patrick, Patricia L.
REGISTRATION NUMBER: 31,284
TELEPHONE: 404-815-6598
TELECOMMUNICATION INFORMATION:
INFORMATION: 404-815-6595 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2132 amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MODIFICATION: none
HYDROPHILIC: no
ANTISENSE: NO N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapien
US-07-864004
Query Match Similarity: 99.1%; Score 12301; DB 1; Length 2332;
Matches 2330; Conservative 1; Identical 1; Gaps 0;
20 AMRTTGLAVSNMKNQSGELADAPRPVPSPTSTVETLTPEVTLFN 79
1 AMRTTGLAVSNMKNQSGELADAPRPVPSPTSTVETLTPEVTLFN 60
60 IAPRPVPMGLCTPTQATQATQVYVYKAAQVNGSAQVQATVQPSQ 139
1 IAPRPVPMGLCTPTQATQATQVYVYKAAQVNGSAQVQATVQPSQ 120
61 IAPRPVPMGLCTPTQATQATQVYVYKAAQVNGSAQVQATVQPSQ 139
1 IAPRPVPMGLCTPTQATQATQVYVYKAAQVNGSAQVQATVQPSQ 120
121 KKKDQVAVPQSTPTVQVAKENPMASDPLATSTVLSVQVLDKSLGLALVCR 180
1 KKKDQVAVPQSTPTVQVAKENPMASDPLATSTVLSVQVLDKSLGLALVCR 160
200 EGSIAEKETQTLFETLLFVAVDEGSMESSTNSLMQDQASAAAPPHQVQVYNR 259
1 EGSIAEKETQTLFETLLFVAVDEGSMESSTNSLMQDQASAAAPPHQVQVYNR 240
181 EGSIAEKETQTLFETLLFVAVDEGSMESSTNSLMQDQASAAAPPHQVQVYNR 240
1 EGSIAEKETQTLFETLLFVAVDEGSMESSTNSLMQDQASAAAPPHQVQVYNR 240
240 SLPLDCKRRHYSVAGTQETPVPSIFTEQPTLVNRRNDALEISPTFIDQTL 319
1 SLPLDCKRRHYSVAGTQETPVPSIFTEQPTLVNRRNDALEISPTFIDQTL 300
241 STPLDCKRRHYSVAGTQETPVPSIFTEQPTLVNRRNDALEISPTFIDQTL 300
1 STPLDCKRRHYSVAGTQETPVPSIFTEQPTLVNRRNDALEISPTFIDQTL 300

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320 MDQGLTSLSSSRNKAQVYVQSGTPEEQDIAKKNNKKNRNDYDQDTRQSDVNP 379
1 MDQGLTSLSSSRNKAQVYVQSGTPEEQDIAKKNNKKNRNDYDQDTRQSDVNP 360
380 DDQNSSTFQISVAKKRRVTHVIAEEDNDQVLAIDQNSSTQVNNPQVIG 439
1 DDQNSSTFQISVAKKRRVTHVIAEEDNDQVLAIDQNSSTQVNNPQVIG 420
361 DDQNSSTFQISVAKKRRVTHVIAEEDNDQVLAIDQNSSTQVNNPQVIG 420
1 DDQNSSTFQISVAKKRRVTHVIAEEDNDQVLAIDQNSSTQVNNPQVIG 420
440 EKRYQVAVNATPTPTQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 499
1 EKRYQVAVNATPTPTQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 480
421 KKKFVPMATPTPTQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 480
1 KKKFVPMATPTPTQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 460
500 TQVPTPTQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 559
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481 TQVPTPTQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 559
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541 MDQGLTSLSSSRNKAQVYVQSGTPEEQDIAKKNNKKNRNDYDQDTRQSDVNP 519
1 MDQGLTSLSSSRNKAQVYVQSGTPEEQDIAKKNNKKNRNDYDQDTRQSDVNP 500
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601 VQDDEPQVSNHNSINQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 560
1 VQDDEPQVSNHNSINQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 540
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721 DQDQDQATLSNNVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 780
1 DQDQDQATLSNNVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 760
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860 LKHSQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 919
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920 TSSQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 979
1 TSSQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 960
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1340 PLEPTPTQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1399
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MEDIAN TYPE: Fropy disk
OPERATING SYSTEM: PC-COS/MS-DOS
SOFTWARE: Relentless Release #1.0, Version #1.25
APPLICATION NUMBER: 05/08/213.133A
FILING DATE: March 11, 1994
PHOTD APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
ATTORNEY/AGENT INFORMATION:
NAME: Publ. Patent L. 284
APPLICATION NUMBER: 1,284
REFERENCE NUMBER: 01/176677
TELEPHONE: 404-572-6508
TELEFAX: 404-572-6508
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 100
TYPE: amino acid
STRANDNESS: single
HYDROPHILIC: YES
HYDROPHETIC: YES
FRAGMENT TYPE: protela
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE: liver
SEQUENCE: liver cDNA sequence

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[illegible][illegible]













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GenCode version 5.1.6  
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(Without alignment) 5100.912 Million call updates/sec

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Scoring table: BLOSUM62

Gap: 10.0, Gapex: 0.5

Search: 440861 seqs, 114592915 residues

Total number of hits satisfying chosen parameters: 440863

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Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	12418	100.0	2351	9	US-10-137-829-4		Sequence 2, App1
2	12301	99.1	2332	9	US-09-597-641-2		Sequence 2, App1
3	12302	99.1	2332	9	US-09-597-641-2		Sequence 2, App1
4	8633	71.1	2319	9	US-10-187-513-6		Sequence 31, App1
5	8078	65.0	2133	9	US-10-187-513-7		Sequence 31, App1
6	7232	58.2	1438	12	US-10-187-513-9		Sequence 31, App1
7	7232	58.2	1438	12	US-10-187-513-9		Sequence 31, App1
8	7232	58.2	1438	12	US-10-187-513-9		Sequence 31, App1
9	7232	58.2	1438	12	US-10-187-513-9		Sequence 31, App1
10	7232	58.2	1438	12	US-10-187-513-9		Sequence 31, App1
11	6123	49.3	1443	9	US-10-187-513-9		Sequence 31, App1
12	2815	22.7	2224	9	US-10-137-829-4		Sequence 14, App1
13	2815	22.7	2224	9	US-10-137-829-4		Sequence 14, App1
14	1333.5	10.7	1160	9	US-10-137-829-4		Sequence 234, App
15	1333.5	10.7	1160	9	US-10-137-829-4		Sequence 234, App
16	1333.5	10.7	1160	9	US-10-137-829-4		Sequence 234, App
17	1333.5	10.7	1160	9	US-10-137-829-4		Sequence 234, App
18	1333.5	10.7	1160	9	US-10-137-829-4		Sequence 234, App
19	1333.5	10.7	1160	9	US-10-137-829-4		Sequence 234, App

## ALIGNMENTS

Result	No.	Score	Match	Length	DB	ID	Description
1	12418	100.0	2351	9	US-10-137-829-4		Sequence 2, App1
2	12301	99.1	2332	9	US-09-597-641-2		Sequence 2, App1
3	12302	99.1	2332	9	US-09-597-641-2		Sequence 2, App1
4	8633	71.1	2319	9	US-10-187-513-6		Sequence 31, App1
5	8078	65.0	2133	9	US-10-187-513-7		Sequence 31, App1
6	7232	58.2	1438	12	US-10-187-513-9		Sequence 31, App1
7	7232	58.2	1438	12	US-10-187-513-9		Sequence 31, App1
8	7232	58.2	1438	12	US-10-187-513-9		Sequence 31, App1
9	7232	58.2	1438	12	US-10-187-513-9		Sequence 31, App1
10	7232	58.2	1438	12	US-10-187-513-9		Sequence 31, App1
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13	2815	22.7	2224	9	US-10-137-829-4		Sequence 14, App1
14	1333.5	10.7	1160	9	US-10-137-829-4		Sequence 234, App
15	1333.5	10.7	1160	9	US-10-137-829-4		Sequence 234, App
16	1333.5	10.7	1160	9	US-10-137-829-4		Sequence 234, App
17	1333.5	10.7	1160	9	US-10-137-829-4		Sequence 234, App
18	1333.5	10.7	1160	9	US-10-137-829-4		Sequence 234, App
19	1333.5	10.7	1160	9	US-10-137-829-4		Sequence 234, App





















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RESULT 8
US Sequence 1.1 Application US/1006091
US Sequence 1.1 Patent No. US61020107701A1
US Sequence 1.1 ORIGINATOR: Geneng Sam
US Sequence 1.1 APPLICANT: Chan, Shan-tuen
US Sequence 1.1 APPLICANT: Katsuy, William
US Sequence 1.1 TITLE OF INVENTION: Depression System for Factor VIII
US Sequence 1.1 FILE REFERENCE: JMS 7755-1
US Sequence 1.1 CURRENT FILING DATE: 2001-12-06
US Sequence 1.1 NUMBER OF SEQ ID NOS: 2
US Sequence 1.1 SEQ ID NO: 1
US Sequence 1.1 SEQ ID NO: 2
US Sequence 1.1 LENGTH: 1438
US Sequence 1.1 ORIGINATOR: Artificial Sequence
US Sequence 1.1 FEATURE: Description of Artificial Sequence: Derived from
US Sequence 1.1 OTHER INFORMATION: Human Factor VIII sequence
US-10-006-091-1

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Beat Local 61.6% Pwd. No. 0
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 ? APPLICANT: Cio, Myung-Sam  
 ? APPLICANT: Kook, Seung-Han  
 ? APPLICANT: Yoo, Jaeha  
 ? TITLE OF INVENTION: Expression System for factor VIII  
 ? CURRENT FILING DATE: 2002-01-15  
 ? CURRENT APPLICATION NUMBER: 05/10/047/257  
 ? SOFTWARE: Patent ver. 2.0  
 ? SEQ ID NO: 1  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? SEQUENCE INFORMATION: Description of Artificial Sequence: Derived from  
 ? OTHER INFORMATION: human factor VIII sequence  
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GenCode version 5.1.6  
Copyright (c) 1995 - 2000 Comagen Ltd.

OR protein - protein search, using pw model

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NP\_000123 2554.87k Million cell updates/sec

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Searched: 113892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 113892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing files: 49 summaries

Database: SwissProt.40.4

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SEQUENCES

Result No.	Score	Match	Length	DB ID	Description
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## RESULT 3

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AC P12261 095243: (Access updates)

DT 01-OCT-1989 (Rel. 12, Created)

DT 15-JUN-2002 (Rel. 41, Last amendment update)

DE Coagulation factor VIII precursor (procoagulant component).

08 Sub specie (P14).

OC Eukaryote; Metazoa; Chordata; Vertebrata; Batracomi;

OC NEB:taxid=65251; Chordata; Batracomi; Salam;

RN [1]

RN SOURCE FROM NA.

RN RECD: 11-01-1996

RN SUBSTENCE OF 705-1573 FROM NA.

RN MEDLINE=6637669; PubMed=5015730.

RN TITLE: A plasma D.D., Of E.C., Martha P., Masley L.C.,

RN "A large region (approximately equal to 95 kbp) of human factor VIII

RN is dispensable for in vitro procoagulant activity."

RN [3] (Rel. 405243, 01-01-1996-39441989).

RN SOURCE OF 322799 FROM NA.

RN RECD: 11-01-1996

RN SUBSTENCE OF 705-1573 FROM NA.

RN MEDLINE=6637669; PubMed=5015730.

RN TITLE: A plasma D.D., Of E.C., Martha P., Masley L.C.,

RN "A large region (approximately equal to 95 kbp) of human factor VIII

RN is dispensable for in vitro procoagulant activity."

RN [3] (Rel. 405243, 01-01-1996-39441989).

RN SOURCE OF 322799 FROM NA.

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RN SUBSTENCE OF 705-1573 FROM NA.

RN MEDLINE=6637669; PubMed=5015730.

RN TITLE: A plasma D.D., Of E.C., Martha P., Masley L.C.,

RN "A large region (approximately equal to 95 kbp) of human factor VIII

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RN SOURCE OF 322799 FROM NA.

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RN SUBSTENCE OF 705-1573 FROM NA.

RN MEDLINE=6637669; PubMed=5015730.

RN TITLE: A plasma D.D., Of E.C., Martha P., Masley L.C.,

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Db 760 1899

Db 1499 1822

Db 1499 1822

Db 1499 1822

Db 1499 1822

Db 1499 1822

Db 1499 1822

Db 1499 1822

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Db 1499 1822

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[illegible][illegible]

[illegible][illegible]

FM	111	REPEAT	1268	1276	2-10.
FM	112	REPEAT	1276	1287	2-11.
FM	113	REPEAT	1287	1295	2-11.
FM	114	REPEAT	1295	1304	2-11.
FM	115	REPEAT	1304	1312	2-11.
FM	116	REPEAT	1312	1322	2-11.
FM	117	REPEAT	1322	1331	2-16.
FM	118	REPEAT	1331	1349	2-16.
FM	119	REPEAT	1349	1358	2-15.
FM	120	REPEAT	1358	1376	2-21.
FM	121	REPEAT	1376	1385	2-22.
FM	122	REPEAT	1385	1404	2-22.
FM	123	REPEAT	1404	1412	2-25.
FM	124	REPEAT	1412	1430	2-25.
FM	125	REPEAT	1430	1441	2-27.
FM	126	REPEAT	1441	1459	2-28.
FM	127	REPEAT	1459	1472	(POTENTIAL).
FM	128	REPEAT	1472	1482	2-30.
FM	129	REPEAT	1482	1493	2-30.
FM	130	REPEAT	1493	1504	2-30.
FM	131	REPEAT	1504	1519	2-30.
FM	132	REPEAT	1519	1530	2-30.
FM	133	REPEAT	1530	1543	2-30.
FM	134	REPEAT	1543	1559	2-30.
FM	135	REPEAT	1559	1576	2-30.
FM	136	REPEAT	1576	1590	2-30.
FM	137	REPEAT	1590	1604	2-30.
FM	138	REPEAT	1604	1620	2-30.
FM	139	REPEAT	1620	1639	2-30.
FM	140	REPEAT	1639	1659	2-30.
FM	141	REPEAT	1659	1680	2-30.
FM	142	REPEAT	1680	1701	2-30.
FM	143	REPEAT	1701	1722	2-30.
FM	144	REPEAT	1722	1742	2-30.
FM	145	REPEAT	1742	1762	2-30.
FM	146	REPEAT	1762	1782	2-30.
FM	147	REPEAT	1782	1804	2-30.
FM	148	REPEAT	1804	1824	2-30.
FM	149	REPEAT	1824	1844	2-30.
FM	150	REPEAT	1844	1864	2-30.
FM	151	REPEAT	1864	1884	2-30.
FM	152	REPEAT	1884	1904	2-30.
FM	153	REPEAT	1904	1924	2-30.
FM	154	REPEAT	1924	1944	2-30.
FM	155	REPEAT	1944	1964	2-30.
FM	156	REPEAT	1964	1984	2-30.
FM	157	REPEAT	1984	2004	2-30.
FM	158	REPEAT	2004	2024	2-30.
FM	159	REPEAT	2024	2044	2-30.
FM	160	REPEAT	2044	2064	2-30.
FM	161	REPEAT	2064	2084	2-30.
FM	162	REPEAT	2084	2104	2-30.
FM	163	REPEAT	2104	2124	2-30.
FM	164	REPEAT	2124	2144	2-30.
FM	165	REPEAT	2144	2164	2-30.
FM	166	REPEAT	2164	2184	2-30.
FM	167	REPEAT	2184	2204	2-30.
FM	168	REPEAT	2204	2224	2-30.
FM	169	REPEAT	2224	2244	2-30.
FM	170	REPEAT	2244	2264	2-30.
FM	171	REPEAT	2264	2284	2-30.
FM	172	REPEAT	2284	2304	2-30.
FM	173	REPEAT	2304	2324	2-30.
FM	174	REPEAT	2324	2344	2-30.
FM	175	REPEAT	2344	2364	2-30.
FM	176	REPEAT	2364	2384	2-30.
FM	177	REPEAT	2384	2404	2-30.
FM	178	REPEAT	2404	2424	2-30.
FM	179	REPEAT	2424	2444	2-30.
FM	180	REPEAT	2444	2464	2-30.
FM	181	REPEAT	2464	2484	2-30.
FM	182	REPEAT	2484	2504	2-30.
FM	183	REPEAT	2504	2524	2-30.
FM	184	REPEAT	2524	2544	2-30.
FM	185	REPEAT	2544	2564	2-30.
FM	186	REPEAT	2564	2584	2-30.
FM	187	REPEAT	2584	2604	2-30.
FM	188	REPEAT	2604	2624	2-30.
FM	189	REPEAT	2624	2644	2-30.
FM	190	REPEAT	2644	2664	2-30.
FM	191	REPEAT	2664	2684	2-30.
FM	192	REPEAT	2684	2704	2-30.
FM	193	REPEAT	2704	2724	2-30.
FM	194	REPEAT	2724	2744	2-30.
FM	195	REPEAT	2744	2764	2-30.
FM	196	REPEAT	2764	2784	2-30.
FM	197	REPEAT	2784	2804	2-30.
FM	198	REPEAT	2804	2824	2-30.
FM	199	REPEAT	2824	2844	2-30.
FM	200	REPEAT	2844	2864	2-30.
FM	201	REPEAT	2864	2884	2-30.
FM	202	REPEAT	2884	2904	2-30.
FM	203	REPEAT	2904	2924	2-30.
FM	204	REPEAT	2924	2944	2-30.
FM	205	REPEAT	2944	2964	2-30.
FM	206	REPEAT	2964	2984	2-30.
FM	207	REPEAT	2984	3004	2-30.
FM	208	REPEAT	3004	3024	2-30.
FM	209	REPEAT	3024	3044	2-30.
FM	210	REPEAT	3044	3064	2-30.
FM	211	REPEAT	3064	3084	2-30.
FM	212	REPEAT	3084	3104	2-30.
FM	213	REPEAT	3104	3124	2-30.
FM	214	REPEAT	3124	3144	2-30.
FM	215	REPEAT	3144	3164	2-30.
FM	216	REPEAT	3164	3184	2-30.
FM	217	REPEAT	3184	3204	2-30.
FM	218	REPEAT	3204	3224	2-30.
FM	219	REPEAT	3224	3244	2-30.
FM	220	REPEAT	3244	3264	2-30.
FM	221	REPEAT	3264	3284	2-30.
FM	222	REPEAT	3284	3304	2-30.
FM	223	REPEAT	3304	3324	2-30.
FM	224	REPEAT	3324	3344	2-30.
FM	225	REPEAT	3344	3364	2-30.
FM	226	REPEAT	3364	3384	2-30.
FM	227	REPEAT	3384	3404	2-30.
FM	228	REPEAT	3404	3424	2-30.
FM	229	REPEAT	3424	3444	2-30.
FM	230	REPEAT	3444	3464	2-30.
FM	231	REPEAT	3464	3484	2-30.
FM	232	REPEAT	3484	3504	2-30.
FM	233	REPEAT	3504	3524	2-30.
FM	234	REPEAT	3524	3544	2-30.
FM	235	REPEAT	3544	3564	2-30.
FM	236	REPEAT	3564	3584	2-30.
FM	237	REPEAT	3584	3604	2-30.
FM	238	REPEAT	3604	3624	2-30.
FM	239	REPEAT	3624	3644	2-30.
FM	240	REPEAT	3644	3664	2-30.
FM	241	REPEAT	3664	3684	2-30.
FM	242	REPEAT	3684	3704	2-30.
FM	243	REPEAT	3704	3724	2-30.
FM	244	REPEAT	3724	3744	2-30.
FM	245	REPEAT	3744	3764	2-30.
FM	246	REPEAT	3764	3784	2-30.
FM	247	REPEAT	3784	3804	2-30.
FM	248	REPEAT	3804	3824	2-30.
FM	249	REPEAT	3824	3844	2-30.
FM	250	REPEAT	3844	3864	2-30.
FM	251	REPEAT	3864	3884	2-30.
FM	252	REPEAT	3884	3904	2-30.
FM	253	REPEAT	3904	3924	2-30.
FM	254	REPEAT	3924	3944	2-30.
FM	255	REPEAT	3944	3964	2-30.
FM	256	REPEAT	3964	3984	2-30.
FM	257	REPEAT	3984	4004	2-30.
FM	258	REPEAT	4004	4024	2-30.
FM	259	REPEAT	4024	4044	2-30.
FM	260	REPEAT	4044	4064	2-30.
FM	261	REPEAT	4064	4084	2-30.
FM	262	REPEAT	4084	4104	2-30.
FM	263	REPEAT	4104	4124	2-30.
FM	264	REPEAT	4124	4144	2-30.
FM	265	REPEAT	4144	4164	2-30.
FM	266	REPEAT	4164	4184	2-30.
FM	267	REPEAT	4184	4204	2-30.
FM	268	REPEAT	4204	4224	2-30.
FM	269	REPEAT	4224	4244	2-30.
FM	270	REPEAT	4244	4264	2-30.
FM	271	REPEAT	4264	4284	2-30.
FM	272	REPEAT	4284	4304	2-30.
FM	273	REPEAT	4304	4324	2-30.
FM	274	REPEAT	4324	4344	2-30.
FM	275	REPEAT	4344	4364	2-30.
FM	276	REPEAT	4364	4384	2-30.
FM	277	REPEAT	4384	4404	2-30.
FM	278	REPEAT	4404	4424	2-30.
FM	279	REPEAT	4424	4444	2-30.
FM	280	REPEAT	4444	4464	2-30.
FM	281	REPEAT	4464	4484	2-30.
FM	282	REPEAT	4484	4504	2-30.
FM	283	REPEAT	4504	4524	2-30.
FM	284	REPEAT	4524	4544	2-30.
FM	285	REPEAT	4544	4564	2-30.
FM	286	REPEAT	4564	4584	2-30.
FM	287	REPEAT	4584	4604	2-30.
FM	288	REPEAT	4604	4624	2-30.
FM	289	REPEAT	4624	4644	2-30.
FM	290	REPEAT	4644	4664	2-30.
FM	291	REPEAT	4664	4684	2-30.
FM	292	REPEAT	4684	4704	2-30.
FM	293	REPEAT	4704	4724	2-30.
FM	294	REPEAT	4724	4744	2-30.
FM	295	REPEAT	4744	4764	2-30.
FM	296	REPEAT	4764	4784	2-30.
FM	297	REPEAT	4784	4804	2-30.
FM	298	REPEAT	4804	4824	2-30.
FM	299	REPEAT	4824	4844	2-30.
FM	300	REPEAT	4844	4864	2-30.
FM	301	REPEAT	4864	4884	2-30.
FM	302	REPEAT	4884	4904	2-30.
FM	303	REPEAT	4904	4924	2-30.
FM	304	REPEAT	4924	4944	2-30.
FM	305	REPEAT	4944	4964	2-30.
FM	306	REPEAT	4964	4984	2-30.
FM	307	REPEAT	4984	5004	2-30.
FM	308	REPEAT	5004	5024	2-30.
FM	309	REPEAT	5024	5044	2-30.
FM	310	REPEAT	5044	5064	2-30.
FM	311	REPEAT	5064	5084	2-30.
FM	312	REPEAT	5084	5104	2-30.
FM	313	REPEAT	5104	5124	2-30.
FM	314	REPEAT	5124	5144	2-30.
FM	315	REPEAT	5144	5164	2-30.
FM	316	REPEAT	5164	5184	2-30.
FM	317	REPEAT	5184	5204	2-30.
FM	318	REPEAT	5204	5224	2-30.
FM	319	REPEAT	5224	5244	2-30.
FM	320	REPEAT	5244	5264	2-30.
FM	321	REPEAT	5264	5284	2-30.
FM	322	REPEAT	5284	5304	2-30.
FM	323	REPEAT	5304	5324	2-30.
FM	324	REPEAT	5324	5344	2-30.
FM	325	REPEAT	5344	5364	2-30.
FM	326	REPEAT	5364	5384	2-30.
FM	327	REPEAT	5384	5404	2-30.
FM	328	REPEAT	5404	5424	2-30.
FM	329	REPEAT	5424	5444	2-30.
FM	330	REPEAT	5444	5464	2-30.
FM	331	REPEAT	5464	5484	2-30.
FM	332	REPEAT	5484	5504	2-30.
FM	333	REPEAT	5504	5524	2-30.
FM	334	REPEAT	5524	5544	2-30.
FM	335	REPEAT	5544	5564	2-30.
FM	336	REPEAT	5564	5584	2-30.
FM	337	REPEAT			

[illegible][illegible]











[illegible][illegible]

















GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: July 2, 2003, 09:37:41; Search time 138 seconds

(without alignment) 350,486 Million cells updates/sec

Title: NP\_000123

Sequence: 1 mlaefactfclficfca.....whalamefgeapdly 2351

Scoring table: gapop 10.0, capex 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Maximum hit seq length: 0

Maximum hit seq length: 2000000000

Post-processing: Maximum Match 10%

Listing first 45 summaries

Database: 1: sp\_archaea

2: sp\_bacteria

3: sp\_fungi.1.1\*

4: sp\_human\*

5: sp\_mammal\*

6: sp\_mammal\*

7: sp\_mammal\*

8: sp\_mammal\*

9: sp\_mammal\*

10: sp\_mammal\*

11: sp\_mammal\*

12: sp\_mammal\*

13: sp\_mammal\*

14: sp\_mammal\*

15: sp\_mammal\*

16: sp\_mammal\*

17: sp\_mammal\*

Result No.	Score	Match	Length	DB ID	Description
1	9433	76	2343	6	018806
2	9447	76	2343	6	062730
3	2819	223	2119	19	090937
4	2819	223	2119	19	090937
5	2768	223	2183	11	088783
6	1382	111	1157	11	095054
7	1382	111	1157	11	095054
8	1382	111	1157	11	095054
9	1382	111	1157	11	095054
10	1382	111	1157	11	095054
11	1382	111	1157	11	095054
12	1382	111	1157	11	095054
13	1382	111	1157	11	095054
14	1382	111	1157	11	095054
15	1382	111	1157	11	095054
16	1382	111	1157	11	095054
17	1382	111	1157	11	095054

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

17	662.5	5.3	480	4	043854	043854	homo sapien
18	626.1	4.1	428	11	039751	039751	homo sapien
19	517.5	4.1	363	6	077718	077718	homo sapien
20	517.5	4.1	363	6	077718	077718	homo sapien
21	488	3.9	339	4	039719	039719	homo sapien
22	469.5	3.8	301	4	039724	039724	homo sapien
23	469.5	3.8	301	4	039724	039724	homo sapien
24	469.5	3.8	301	4	039724	039724	homo sapien
25	469.5	3.8	301	4	039724	039724	homo sapien
26	469.5	3.8	301	4	039724	039724	homo sapien
27	469.5	3.8	301	4	039724	039724	homo sapien
28	469.5	3.8	301	4	039724	039724	homo sapien
29	469.5	3.8	301	4	039724	039724	homo sapien
30	469.5	3.8	301	4	039724	039724	homo sapien
31	469.5	3.8	301	4	039724	039724	homo sapien
32	469.5	3.8	301	4	039724	039724	homo sapien
33	469.5	3.8	301	4	039724	039724	homo sapien
34	469.5	3.8	301	4	039724	039724	homo sapien
35	469.5	3.8	301	4	039724	039724	homo sapien
36	469.5	3.8	301	4	039724	039724	homo sapien
37	469.5	3.8	301	4	039724	039724	homo sapien
38	469.5	3.8	301	4	039724	039724	homo sapien
39	469.5	3.8	301	4	039724	039724	homo sapien
40	469.5	3.8	301	4	039724	039724	homo sapien
41	469.5	3.8	301	4	039724	039724	homo sapien
42	469.5	3.8	301	4	039724	039724	homo sapien
43	469.5	3.8	301	4	039724	039724	homo sapien
44	469.5	3.8	301	4	039724	039724	homo sapien
45	469.5	3.8	301	4	039724	039724	homo sapien

## ALIGNMENTS

1	018806	PRELIMINARY; FR; 2343 AA.
2	018806	PRELIMINARY; FR; 2343 AA.
3	018806	PRELIMINARY; FR; 2343 AA.
4	018806	PRELIMINARY; FR; 2343 AA.
5	018806	PRELIMINARY; FR; 2343 AA.
6	018806	PRELIMINARY; FR; 2343 AA.
7	018806	PRELIMINARY; FR; 2343 AA.
8	018806	PRELIMINARY; FR; 2343 AA.
9	018806	PRELIMINARY; FR; 2343 AA.
10	018806	PRELIMINARY; FR; 2343 AA.
11	018806	PRELIMINARY; FR; 2343 AA.
12	018806	PRELIMINARY; FR; 2343 AA.
13	018806	PRELIMINARY; FR; 2343 AA.
14	018806	PRELIMINARY; FR; 2343 AA.
15	018806	PRELIMINARY; FR; 2343 AA.
16	018806	PRELIMINARY; FR; 2343 AA.
17	018806	PRELIMINARY; FR; 2343 AA.
18	018806	PRELIMINARY; FR; 2343 AA.
19	018806	PRELIMINARY; FR; 2343 AA.
20	018806	PRELIMINARY; FR; 2343 AA.
21	018806	PRELIMINARY; FR; 2343 AA.
22	018806	PRELIMINARY; FR; 2343 AA.
23	018806	PRELIMINARY; FR; 2343 AA.
24	018806	PRELIMINARY; FR; 2343 AA.
25	018806	PRELIMINARY; FR; 2343 AA.
26	018806	PRELIMINARY; FR; 2343 AA.
27	018806	PRELIMINARY; FR; 2343 AA.
28	018806	PRELIMINARY; FR; 2343 AA.
29	018806	PRELIMINARY; FR; 2343 AA.
30	018806	PRELIMINARY; FR; 2343 AA.
31	018806	PRELIMINARY; FR; 2343 AA.
32	018806	PRELIMINARY; FR; 2343 AA.
33	018806	PRELIMINARY; FR; 2343 AA.
34	018806	PRELIMINARY; FR; 2343 AA.
35	018806	PRELIMINARY; FR; 2343 AA.
36	018806	PRELIMINARY; FR; 2343 AA.
37	018806	PRELIMINARY; FR; 2343 AA.
38	018806	PRELIMINARY; FR; 2343 AA.
39	018806	PRELIMINARY; FR; 2343 AA.
40	018806	PRELIMINARY; FR; 2343 AA.
41	018806	PRELIMINARY; FR; 2343 AA.
42	018806	PRELIMINARY; FR; 2343 AA.
43	018806	PRELIMINARY; FR; 2343 AA.
44	018806	PRELIMINARY; FR; 2343 AA.
45	018806	PRELIMINARY; FR; 2343 AA.

Db	1	NOVELTCEGCELLAPESIAKTRKYTLDAVEJLWESQSDJLMLADITFSSVWSPSLP	60
Db	60	MSWVYATKLEWFFMLPESIAKTRKYTLDAVEJLWESQSDJLMLADITFSSVWSPSLP	119
Db	61	TSYATKLEWFFMLPESIAKTRKYTLDAVEJLWESQSDJLMLADITFSSVWSPSLP	120
Db	120	VONWYATKLEWFFMLPESIAKTRKYTLDAVEJLWESQSDJLMLADITFSSVWSPSLP	179
Db	121	VONWYATKLEWFFMLPESIAKTRKYTLDAVEJLWESQSDJLMLADITFSSVWSPSLP	180
Db	122	VONWYATKLEWFFMLPESIAKTRKYTLDAVEJLWESQSDJLMLADITFSSVWSPSLP	239
Db	181	VONWYATKLEWFFMLPESIAKTRKYTLDAVEJLWESQSDJLMLADITFSSVWSPSLP	238
Db	239	-----	299
Db	240	-----	359
Db	359	-----	419
Db	419	-----	479
Db	479	-----	539
Db	539	-----	599
Db	599	-----	659
Db	659	-----	719
Db	719	-----	779
Db	779	-----	839
Db	839	-----	899
Db	899	-----	959
Db	959	-----	1019
Db	1019	-----	1079
Db	1079	-----	1139
Db	1139	-----	1199
Db	1199	-----	1259
Db	1259	-----	1319
Db	1319	-----	1379
Db	1379	-----	1439
Db	1439	-----	1499
Db	1499	-----	1559
Db	1559	-----	1619
Db	1619	-----	1679
Db	1679	-----	1739
Db	1739	-----	1799
Db	1799	-----	1859
Db	1859	-----	1919
Db	1919	-----	1979
Db	1979	-----	2039
Db	2039	-----	2099
Db	2099	-----	2159
Db	2159	-----	2219
Db	2219	-----	2279
Db	2279	-----	2339
Db	2339	-----	2399
Db	2399	-----	2459
Db	2459	-----	2519
Db	2519	-----	2579
Db	2579	-----	2639
Db	2639	-----	2699
Db	2699	-----	2759
Db	2759	-----	2819
Db	2819	-----	2879
Db	2879	-----	2939
Db	2939	-----	2999

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01	766	AGNAYEVECTOPE - DAYEVEYED -	CHETAKOPEI -	701
02	777	APPENDREKTOPEINPAKJONVASSOLLMALNORPHIGLOSSQJANETTS		816
03	788	NETKEEPPAN -		816
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07	947	FLODDOLPEJESKJESSEN -	LANATQJEFJES -	793
08	957	LENNESJOLPEJESKJESSEN	LENNESJOLPEJESKJESSEN	793
09	974	LENNESJOLPEJESKJESSEN	LENNESJOLPEJESKJESSEN	793
10	974	LENNESJOLPEJESKJESSEN	LENNESJOLPEJESKJESSEN	793
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12	974	LENNESJOLPEJESKJESSEN	LENNESJOLPEJESKJESSEN	793
13	974	LENNESJOLPEJESKJESSEN	LENNESJOLPEJESKJESSEN	793
14	974	LENNESJOLPEJESKJESSEN	LENNESJOLPEJESKJESSEN	793
15	974	LENNESJOLPEJESKJESSEN	LENNESJOLPEJESKJESSEN	793
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61	974	LENNESJOLPEJESKJESSEN	LENNESJOLPEJESKJESSEN	793
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81	974	LENNESJOLPEJESKJESSEN	LENNESJOLPEJESKJESSEN	793
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99	974	LENNESJOLPEJESKJESSEN	LENNESJOLPEJESKJESSEN	793
100	974	LENNESJOLPEJESKJESSEN	LENNESJOLPEJESKJESSEN	793

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80 SOURCE 2224 Mz: 251673 MW: 1011080V6900LAA CR64.

Query Match 22.7% Score 2813.5 Db 4: Length 2244:

Beet Local Similarity 30.5% Prod. No. 3.2e-135: Index 507: Gape 77:

Matches 767: Comitative 389: Nucleotide 832: Indels 507: Gaps 77:

22 BRYTJAVELSVNBSQSDLEFLVAVNPPVPSVPSVSV-XTKTLVPSFQTLN 80

32 KQTYMNOGISTPFRP-----PSSSLALVSGTGLVETRETF PK 75

81 XHPPNKKLQDTQVQVQVQVTLTANSPSVSVANVSTVSTVSTVSTVSTV 140

76 EKQSTISGLDPLVAVNGLVAVNKKVAPSLHVGQVTKKSLVSTVSTVSTV 135

141 EKDDQVPPQSTVQVAVKKNQVADGLVSTVSTVSTVSTVSTVSTVSTV 130

136 KNDQVAVNPPVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 155

201 GSAKQVTLK-PLVAVNPPVPSVPSVPSVPSVPSVPSVPSVPSVPSV 258

196 QSTVQV 239

259 NSLQQLDCKRQVAVNPPVPSVPSVPSVPSVPSVPSVPSVPSVPSV 218

240 QTPVQV 299

319 LMDQVQ 378

300 VQPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 342

379 TQDQVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 388

343 QSTVQV 387

429 GATKQV 395

388 GATKQV 446

447 PLOVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 502

550 RVSQVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 528

503 RVSQVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 562

610 LQSTVQV 468

563 INQVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 422

669 STVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 528

623 TLPQVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 682

729 SCQV 762

643 KC-----PQDQVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 739

762 SQNSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 820

740 RNSL-NDQVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 810

821 GLS-----LSTQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 869

782 KSTVQV 914

870 P-----SSQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 936

839 PLQV 887

915 -AGQVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 967

888 KQV 947

968 -----SQD-----LMDQVPSVPSVPSVPSVPSVPSVPSVPSVPSV 999

948 BLKQSTVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 1007

1000 PLVQV 1057

1008 SLQV 1087

1058 FQV 1115

1056 FQV 1091

1116 FQV 1173

1092 GQV 1138

1174 GQV 1221

1139 -HSDQVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 1187

1222 TLDQV 1280

1198 KSTVQV 1240

1281 -----KSTVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1337

1241 SPQV 1273

1338 RPLQV 1393

1374 -HSDQVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 1438

1379 TQVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 1453

1329 TLDQV 1373

1434 LQV 1510

1374 -----HSDQVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 1426

1511 VQLQV 1556

1427 KQV 1603

1457 KQV 1603

1481 S-----PQDQVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 1595

1604 KQV 1663

1536 -----PQDQVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 1595

1664 RQV 1718

1536 -----DQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1583

1713 IAVQV 1773

1584 LQV 1639

1774 KQV 1835

1640 KQV 1699

1826 VQV 1885

1700 VQV 1759

1866 KQV 1945

1760 SQV 1813

[illegible][illegible]







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DB	PROSTATE: PS00001, MULTIDRUG RESISTANCE 1	DB	736	-----HAIETLHND-----	104
DB	SEQUENCE: 1157 Aa, 12993 Wb, 0656673512ED, CIRC4.	DB	999	GRALLITONLFRYSLSLKTWTSSNKAHNTKTHLDQPSLIDNSVYQWGLLSOTPF	1078
DB	Query Match	DB	745	KTPTPLDLDHNDQNNKNNLRLNMSKSTKSNKNDVQKQKTPDIPDQNSPFFKA	1118
DB	Heat Local Similarity	DB	745	-----TCDSN-----	750
DB	Matches: 417 Conservative: 176; Mismatches: 406; Indels: 1064; Gaps: 31;	DB	1119	LEPSSN-NGHTRKNSLSNSQDQPSKQVSLQDPSVSDQNSLSEKKNVYQSGFK	1178
DB	11.0% Score: 1366; DB: 11; Length: 1371	DB	751	-----N-----	751
DB	20 AMRTATLSESDPHSDSELEPDAKREPKVSE-----PFSVSTVETLTPFV	DB	1179	DGLKDNTPSSRNLTFLNLALHNTTNGKATQDELKKEKTLQDNVYLDLHTVNG	1218
DB	84 GTTTELEKEMFADQLDLKALNKGDDVLLILKNNKSPRTTHVQVTEKSSKSLVY	DB	752	-----VSI-----	751
DB	136 QGQKREDDVYRGSSSTVWQVLEKNGMAYSDGLATYSLSVQWGLDGL	DB	1239	THNNKALFLSTPDVNSQVQKAVVLDQPSLNSNTPKRTKTHSKGSEKMLD	1298
DB	144 QSGQKLDADVPSQSGVSHVNSLTPSGMTPALMDLILVNSHVAQVADLQGL	DB	752	-----	751
DB	186 LVPDSLS-----AKETQTLKFTLAVPDSKDNIE-----TNSMDPDAKSL	DB	1359	LDNGTQVLEKATCTSTSPVSDQVYQSKNLQGLRSLLESTLEKNTLVDSQV	1398
DB	204 LKNNKLDQNNRQNNQNNVFLDQVSDKNNKNDQNNATQNNASVNNQPP	DB	752	-----EEL-----	754
DB	246 AKKKKATVNGVNSLLELLQGNKSVNMYVLDGTTPVPSLTPLEKRTLVNNQKSL	DB	1359	KNNKNNLTPTSTLDTPKRNKATQSPASQCTNSHSITQNNSPVJANVSFSL	1418
DB	284 QSNRDLAINGVQNLPELQNGQVHLEKSNQNDVETAFHQGTSLNRTDQV	DB	755	-----VNSK-----	761
DB	324 HLEPVTYNNKQVSKSTMLACVYNNHLSQNNATKQSSNNQPV	DB	1419	RPVTVQVNSNLSUPLASVTKQSDQVDSNPVQAKNNKSLALTLTPNQV	1478
DB	366 DDQLDSNDVYQDQNSPSTQISNAKKEKTVNHTLAESSEVPAVLAQPS	DB	762	-----	761
DB	373 TQDLS-----ATQGLQKELQNNP-----SREKST	DB	1479	GSGLSTNNVYKVVNTVLPKQVKTSGVVELFVHTVQKDLPTSTNQSNNLD	1538
DB	426 KTE-----QTNQPKQITKRTVYNNATQDTEKTAQNNR-----QTLQPLQ	DB	1539	LDQSLQGLQALIMNNKNNKQVPLVAVNSNATPSLQPLAMNNQVQTPRE	1598
DB	403 QSLKESQDQVQKSSRLDQVWYVYVADQDFQRLHREBETLQDLPVLA	DB	769	-----DSTVYF	768
DB	475 PQQDGLLLEKNNKSRVNTYNGLTQVRYLSEMLPKV-----RLKQPLMG	DB	1599	WQSKSPSTKPKKRTQTLSEKNSNNMLANINQKPELETVYNNQDFPRLSQN	1658
DB	463 SVQDTQVYVNAQPSLQHPNQ-----FRLSSDQVYNNQSTFNNKSP	DB	770	-----SNNQGL-----	776
DB	526 EELKTVYVNAQPSLQHPNQ-----FRLSSDQVYNNQSTFNNKSP	DB	1659	PVYNNQKRTQDQSDQDQDQDQVTSNKEPQDTPEDQNSQNSQKTHNF	1718
DB	512 KRTVYVNAQPSLQHPNQ-----FRLSSDQVYNNQSTFNNKSP	DB	777	-----	776
DB	586 NKKRTVYVNAQPSLQHPNQ-----FRLSSDQVYNNQSTFNNKSP	DB	1719	IANVRLNDQSSSPVNLNNAQSGVQKVVQDFTNSQDTEKREBNNL	1778
DB	640 VQPSLQVQVNAQPSLQHPNQ-----FRLSSDQVYNNQSTFNNKSP	DB	1779	GGTIANVRLNDQSSSPVNLNNAQSGVQKVVQDFTNSQDTEKREBNNL	1837
DB	656 LKNNKLDADVPSQSGVSHVNSLTPSGMTPALMDLILVNSHVAQVADLQGL	DB	810	GPGLKKEGVDLLVYQNSKNSPSSIHAVQVSSSTQVQAL-----PQVLTQVNN	862
DB	699 NKKNNKLDADVPSQSGVSHVNSLTPSGMTPALMDLILVNSHVAQVADLQGL	DB	1818	VQNNHVAQVQDQNNKAVYQNSKNSPSSIHAVQVSSSTQVQAL-----PQVLTQVNN	1897
DB	686 KQNNKLDADVPSQSGVSHVNSLTPSGMTPALMDLILVNSHVAQVADLQGL	DB	863	IPKNNQVQSDQNNKAVYQNSKNSPSSIHAVQVSSSTQVQAL-----PQVLTQVNN	922
DB	729 NKKNNKLDADVPSQSGVSHVNSLTPSGMTPALMDLILVNSHVAQVADLQGL	DB	1898	FTPTPEKSTVPSNNKSK-NQKQVQNNQDQVFTNNKSTVPSNNKSTVPSNNK	952
DB	755 KQNNKLDADVPSQSGVSHVNSLTPSGMTPALMDLILVNSHVAQVADLQGL	DB	923	LEPSSN-NGHTRKNSLSNSQDQPSKQVSLQDPSVSDQNSLSEKKNVYQSGFK	986
DB	819 PQLSSLDQVNAQPSLQHPNQ-----FRLSSDQVYNNQSTFNNKSP	DB	1937	QNLNKLKNNKSTVPSNNKSTVPSNNKSTVPSNNKSTVPSNNKSTVPSNNK	2016
DB	879 NKKNNKLDADVPSQSGVSHVNSLTPSGMTPALMDLILVNSHVAQVADLQGL	DB	983	EVAVNNKLDADVPSQSGVSHVNSLTPSGMTPALMDLILVNSHVAQVADLQGL	1042
DB	733 -----VY-----	DB	2017	VELGLHNNKSTVPSNNKSTVPSNNKSTVPSNNKSTVPSNNKSTVPSNNK	2017





[illegible]

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619 LMAPFBSBVDCLTTOHOTOOMKQTTVNC-----KQFBOV-----720
Oy 757 FBSBSSNSBFBTNOJFMTATETEDTETKTFPANTPARKONVSSSLMLLNG 816
Db 721 -----720
Oy 817 PFMQSLSDQAKETFBSDYQVSLDKNNLSBHTFPLDLSNOGWYTFYSGL 876
Db 721 -----720
Oy 877 MLKBTGLTATKLFBSSTNNLSSTFSLMLACTGTSGLPMSVPTSL 936
Db 721 -----720
Oy 937 FTTLFBSSTFBSQSLBSBENDKTLBSGMSBSSMCMVSTFBSLPMGR 996
Db 721 -----720
Oy 997 MGRALTLMDALFVSSSLFNTSSMNAKNTFTDPLBNGSPVWMLDSTP 1056
Db 727 FVYLA-----722
Oy 1057 FSKVYPLTIDMDKDMATMLBNGNTTSSMNMVQKFKSPFDDKQDMSTP 1116
Db 733 -----732
Oy 1117 FMELFBSBNTQFQFNSLMSQSPQFVSLGPFSVCQWTFSSNTVNGVSE 1176
Db 733 -----732
Oy 1177 FKVQFLMFWPFSBMLPLTMDLNBHNTNTEKTDIEIKETLQDSVLTQV 1236
Db 733 -----732
Oy 1237 FCTNNKMLLSTFNOVQSSDQXAPVLOPFSLSNDTWTAKTNAFKKSEEN 1296
Db 733 -----741
Oy 1297 VERMD--TSP-----741
Oy 1297 FDLQWQTOVETKCTTBSFWSQWVQSSAKALQFLPTELEKELTIVDS 1356
Db 742 -----742
Oy 1357 FQSSKNNMLPSTPDQDLYNHEKQALTOFSLDCLTBSLTPANSTPL 1416
Db 743 HDBHBNH-----752
Oy 1417 SHPLTFLVLEJDNSSFLPAKTKKQSVSSRFLQATKNNLSLTLTNTDOR 1476
Db 753 -----762
Oy 1477 FNSQSLTANSTNTKRWVWVPLPPLPMTGNTLWVHTYQDLPFTSSNGPBN 1536
Db 763 -----762
Oy 1537 LQVMSGLQDQGLAKNNBNBQVPLVPLVMTSSAATPFLKDLMDHMDTQIK 1596
Db 763 -----762
Oy 1597 FEMKQSBSEKFAKQDITLMLDSMMLALNBSQNEPLVYKNGHSELS 1656
Db 763 -----762
Oy 1657 QNVYKLNQKBTFTTLAGQDELTDTOTLTSBKKEDDTDNDONGSPSPONTN 1716
Db 763 -----766
Oy 1717 FVPAFLBMYQNSHTPLAKMAGSSQVQVQVQVQVQVQVQVQVQVQV 1776
Db 767 FVFSQ-----776
Oy 1777 LPLFLBMDYVNTFQNSQFSTSLSEBQDQKQDQKQKQKQKQKQKQKQ 1833
Db 801 LQDPLMDQVQVAKVAKMNSBFTSLA-----BKVNSSTVFTLQSVAT 150

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Oy 1834 YFNTQVHMAFTEDESCAKMAYFSQDLSQVSDLSQVLAQVLAQVLAQV 1890
Db 851 LMAPFBSBVDCLTTOHOTOOMKQTTVNC-----KQFBOV-----905
Oy 1891 TVQFALPTFTEDESKPTFENKMKMAQCNQDQFTEKFEPLANQVLDLQF 1950
Db 906 KMDSTSLVYDSSBNVYLDQNTKTSNDRKQVONBSELENNKMLKQVQVQV 965
Oy 1951 LMAPQDQFVYVLTQVNSVHTFSSQVQVQVQVQVQVQVQVQVQVQV 2010
Db 966 LVMQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1025
Oy 2011 KMDQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1087
Db 1026 TQFQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1097

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RESULT 11  
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 DT 01-MAY-1999 (PRELIMINARY, 12, Last sequence update)  
 DT 01-DEC-2001 (PRELIMINARY, 19, Last annotation update)  
 OS Ovis aries (sheep).  
 OC Buiroids: Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi;  
 OC Bovidae: Caprinae: Ovis  
 NCBI\_TaxID=9940;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER; 106; DMS04-1045245;  
 RA Lockhart, P.J.; Mercer, J.P.B.;  
 DT BML: AB14814; AB04477.1;  
 DR HSS: P0450; IBCV: Cn: Ovis aries;  
 DR InterPro: IPR00135; Cn: Ovis aries;  
 DR PROSITE: PS00079; Cn: Ovis aries;  
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 SEQUENCE: 1048 AM; 119125 MB; 925167049CDB CDS64;  
 Query Match 9.84; score 1201.5; D6.6; length 1048;  
 Best Local Similarity: 19.0%; Pval: No. 1.1e-62;  
 Matches 93; Conservative 164; Mismatches 421; Indels 1075; Gaps 31;  
 9 FFLC--LPC--FSAFVYLVLESHQVQKSLG--LQVAPVPRVPSKSPFN 60  
 4 FLLTFLVLSQVSKMKNITLIIILIIIIIIIIIIIIIIIIIIIIIIIIIIII 62  
 61 TSVKATLTFEFLDPLVAPRPNQGLDQVQVQVQVQVQVQVQVQVQVQVQV 110  
 63 IGVVATLTFEFLDPLVAPRPNQGLDQVQVQVQVQVQVQVQVQVQVQVQV 122  
 120 TKNLMDQDQV 130  
 183 IGVVATLTFEFLDPLVAPRPNQGLDQVQVQVQVQVQVQVQVQVQVQVQV 242  
 184 IGVVATLTFEFLDPLVAPRPNQGLDQVQVQVQVQVQVQVQVQVQVQVQV 250  
 243 FAKDQV 299  
 291 BQFVQV 350









